

-continued

Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
	35						40					45			
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
	50					55					60				
Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His
65					70					75				80	
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys
			85						90					95	
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln
			100					105					110		
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu
	115					120						125			
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro
	130					135					140				
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn
145					150					155				160	
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu
				165					170					175	
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val
			180					185					190		
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln
	195						200				205				
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
	210					215									

1-46. (canceled)

47. A method of treating a subject having an epidermal growth factor 2+ (HER2+) tumor that expresses HER2 at a 2+ level or lower as determined by immunohistochemistry (IHC), the method comprising administering to the subject an effective amount of a combination of a first and a second monovalent antigen-binding construct,

a) wherein the first and second monovalent antigen-binding constructs are distinct and each comprises a single antigen-binding polypeptide construct and a dimeric Fc comprising a first Fc polypeptide and a second Fc polypeptide each comprising a CH2 sequence and a CH3 sequence, the dimeric Fc coupled, with or without a linker, to the antigen-binding polypeptide construct, and wherein the first monovalent antigen-binding construct and the second monovalent antigen-binding construct is each selected from the group consisting of constructs 1 through 5, wherein:

- i) construct 1 comprises an H-CDR1 comprising the sequence set forth in SEQ ID NO:179, an H-CDR2 comprising the sequence set forth in SEQ ID NO:183, an H-CDR3 comprising the sequence set forth in SEQ ID NO:181, an L-CDR1 comprising the sequence set forth in SEQ ID NO:245, an L-CDR2 comprising the sequence set forth in SEQ ID NO:249, and an L-CDR3 comprising the sequence set forth in SEQ ID NO:247, and
- ii) construct 2 comprises an H-CDR1 comprising the sequence set forth in SEQ ID NO:195, an H-CDR2 comprising the sequence set forth in SEQ ID NO:199, an H-CDR3 comprising the sequence set forth in SEQ

ID NO:197, an L-CDR1 comprising the sequence set forth in SEQ ID NO:245, an L-CDR2 comprising the sequence set forth in SEQ ID NO:249, and an L-CDR3 comprising the sequence set forth in SEQ ID NO:247, and

- iii) construct 3 comprises an H-CDR1 comprising the sequence set forth in SEQ ID NO:273, an H-CDR2 comprising the sequence set forth in SEQ ID NO:277, an H-CDR3 comprising the sequence set forth in SEQ ID NO:275, an L-CDR1 comprising the sequence set forth in SEQ ID NO:89, an L-CDR2 comprising the sequence set forth in SEQ ID NO:93, and an L-CDR3 comprising the sequence set forth in SEQ ID NO:91, and
- iv) construct 4 comprises an H-CDR1 comprising the sequence set forth in SEQ ID NO:225, an H-CDR2 comprising the sequence set forth in SEQ ID NO:229, an H-CDR3 comprising the sequence set forth in SEQ ID NO:227, an L-CDR1 comprising the sequence set forth in SEQ ID NO:217, an L-CDR2 comprising the sequence set forth in SEQ ID NO:221, and an L-CDR3 comprising the sequence set forth in SEQ ID NO:219, and
- v) construct 5 comprises an H-CDR1 comprising the sequence set forth in SEQ ID NO:101, an H-CDR2 comprising the sequence set forth in SEQ ID NO:105, an H-CDR3 comprising the sequence set forth in SEQ ID NO:103, an L-CDR1 comprising the sequence set forth in SEQ ID NO:109, an L-CDR2 comprising the